## Diamond from graphite

SIR - Daedalus is preternaturally sensitive to the scientific atmosphere. Having predicted ${ }^{1}$ the larger buckminsterfullerenes - cages of graphite-like sheets, with 12 five-membered rings among the hexagons to permit topological closure into a shell - he now goes on to consider graphite foam ${ }^{2}$. We have recently been building models of periodic minimal surfaces ${ }^{3}$ from graphite-like sheets. Because minimal surfaces have zero mean curvature and the gaussian curvature (the product of the two principal curvatures; one positive and one negative for a saddle-shaped surface) is everywhere non-positive, it is necessary to introduce rings of more than six carbon atoms (for $s p^{2}$ bonding). We substitute a few rings of eight for hexagons and find that this can be done with surprisingly little strain. The octagons are puckered with bond angles close to $120^{\circ}$, and sit appropriately on positions of symmetry $\overline{4 m}$.

The simplest surface is shown in the figure. The P-surface has been covered with a graphite net of 12 octagons and 80 hexagons. There are 96 asymmetric units


The periodic minimal surface, called the P-surface, of H. A. Schwarz decorated with a graphite mesh. This unit cell, of space group Im3m, repeats by translation. Rings of eight allow the gaussian curvature to be negative, that is, saddle-shaped.
in the cell shown, which has a repeat distance about ten times the bond length. The mean coordination number is 6.26 .

The diamond D-surface of H . A. Schwarz has been built with 8 tetrahedral units per cell, so that there are 768 carbon atoms per face centred cubic unit cell. It uses the same $30^{\circ}-45^{\circ}-90^{\circ}$ patches as the P -surface illustrated. Here they are tetrahedral joints, where four tubes meet tetrahedrally, each consisting of six octagons and 40 hexagons so that the mean coordination number is also 6.26. (The mean coordination number for a plane net must be 6 and for the spherical shell of buckminsterfullerene,
which has a positive gaussian curvature, it is 5.625 .) The same tetrahedral units may also be joined hexagonally. Thus, paradoxically, we can make the diamond structure out of graphite.

The P-surface of Schwarz has also been built with 432 atoms per cell in 200 hexagons and 12 octagons using a larger patch, so that the mean coordination number is 6.11 . Here the unit cell edge is about 15 times the bond distance.

In each case a plane triangle from the graphite net with angles $30^{\circ}-60^{\circ}-90^{\circ}$ is curved so that $60^{\circ}$ vertices become $45^{\circ}$
and eight fit together to give an octagon. The triangle can be chosen in several ways, and other surfaces can be similarly decorated.

Thus, we find that a variety of ordered graphite foams look quite possible. The question is how to synthesize them.

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## Mitochondrial protein charge

SIR - Most mitochondrial proteins are imported from the cytosol and are targeted into the organelle by an aminoterminal presequence which is removed during the importation process ${ }^{1,2}$. Within the organelle they are subject to specific local conditions, such as higher pH and higher calcium-ion concentration than in the cytosol, and to interactions with a specific subset of cellular proteins. Thus, the question arises of whether evolutionary pressure has endowed mitochondrial proteins with specialized structural features. The observation that the authentic precursor of mitochondrial aspartate aminotransferase is imported four times faster than a chimaeric construct consisting of the same presequence fused to the much less basic homologous cytosolic isoenzyme ${ }^{3}$ sug-
gests that the pI value could be such a compartment-specific trait. The pIs of both mitochondrial and cytosolic proteins vary considerably (see refs 4,5), making comparisons difficult. But by comparing pIs in pairs of similar mitochondrial and cytosolic isoproteins, we find that, with few exceptions, the pI of the mitochondrial isoprotein is higher than that of its cytosolic counterpart, the average difference being 1.4.

The average pI values of the mitochondrial and cytosolic isoproteins are 7.2 and 5.8 , respectively (see table). Seven of the eleven isoprotein pairs show the corresponding positive pI difference ( $\Delta \mathrm{pI}$ ) unambiguously (regardless of the analysed species or tissue). Identical pIs were reported for phosphoenolpyruvate carboxykinase from chicken

| ISOELECTRIC POINTS OF HOMOLOGOUS MITOCHONDRIAL AND CYTOSOLIC ISOENZYMES |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: |
| Enzyme | Source | pl of isoe mitochondrial | zyme: <br> cytosolic | Difference |
| Aconitate hydratase | Pig heart, liver, kidney | 7.5 | 5.4 | 2.1 |
| Adenylate kinase | Pig heart | 4.7-7.5, 9.3 | 4.7-7.5, 9.3 | 0.0 |
|  | Rat liver | 8.0 | 7.5 | 0.5 |
| Alanine aminotransferase | Bovine brain | 7.2 | 5.2 | 2.0 |
|  | Pig liver, kidney | 8.0-9.0 | 5.3-6.0 | 2.9 |
| Aldehyde dehydrogenase | Sheep liver | 6.6 | 6.2 | 0.4 |
|  | Sheep liver | 5.22-5.76 | 5.2 | 0.3 |
|  | Rat liver | 5.6 | 5.8,8.5 | -1.6 |
| Aspartate aminotransferase | Human liver | 9.6 | 5.22-5.62 | 3.2 |
|  | Chicken heart | 9.0-9.5 | 6.7 | 2.5 |
|  | Rabbit liver | 9.6 | 5.3 | 4.3 |
| Creatine kinase | Chicken heart, brain | 9.3-9.5 | 7.4,7.5 | 2.0 |
|  |  | 8.5-8.9 | 6.1,6.5 | 2.4 |
| Fumarase | Human fibroblasts | 5.65-6.8 | 5.5,5.6 | 0.7 |
| 3-Hydroxy-3-methylglutaryi coenzyme A synthetase | Chicken liver | 7.2 | 4.8,6.7 | 1.5 |
| Malate dehydrogenase | S. cerevisae | 6.8 | 6.75-7.1 | -0.1 |
|  | N. crassa | 7.0,7.5 | 5.6 | 1.6 |
|  | Rabbit heart | 9.0,9.2,9.5 | 5.1 | 4.1 |
|  | Pig liver | 10 | 5.1 | 4.9 |
| Phosphoenolpyruvate carboxykinase | Chicken liver | 5.0 | 5.0 | 0.0 |
| Serine hydroxymethyltransferase | Rat liver | 5.3 | 4.9 | 0.4 |
| Average (s.e.)* |  | 7.2 (0.4) | 5.8 (0.2) | 1.4 (0.4) |

The table contains all pairs of homologous mitochondrial and cytosolic isoenzymes with known isoelectric points that we could find. References reporting the pl values and the homology of the two isoenzymes (except for alanine aminotransferase and aconitate hydratase) are available on request.
*Each protein was given equal weight in the calculation by using the mean of the values obtained for different sources. A difference of the means test indicates the mean values of the pls to be significantly different with $P<0.02$.

